



SEQUENCE LISTING

(1) GENERAL INFORMATION:

(i) APPLICANTS:

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(ii) TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR EFFECTING THE LEVELS OF HIGH DENSITY LIPOPROTEIN (HDL) CHOLESTEROL AND APOLIPOPROTEIN AI, VERY LOW DENSITY LIPOPROTEIN (VLDL) CHOLESTEROL AND LOW DENSITY LIPOPROTEIN (LDL) CHOLESTEROL

(iii) NUMBER OF SEQUENCES: 27

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(C) CITY: Philadelphia

(D) STATE: PA

(E) COUNTRY: USA

(F) ZIP: 19107

(v) COMPUTER READABLE FORM:

(A) MEDIUM TYPE: Floppy disk

(B) COMPUTER: IBM PC compatible

(C) OPERATING SYSTEM: PC Windows 95

(D) SOFTWARE: Microsoft Word converted to ASCII

(vi) CURRENT APPLICATION DATA:

(A) APPLICATION NUMBER: 09/277,401

(B) FILING DATE: March 26, 1999

(C) CLASSIFICATION:

(viii) ATTORNEY/AGENT INFORMATION:

(A) NAME: Yao, Gene J.

(B) REGISTRATION NUMBER: 47,193

(C) REFERENCE/DOCKET NUMBER: 22,944 C USA

(ix) TELECOMMUNICATION INFORMATION:

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(2) INFORMATION FOR SEQ ID NO:1:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 367 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

(A) NAME/KEY: CDS

(B) LOCATION: 22..180

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

GAATTCGGCT TGATCAATCG C	TTC AAA AAG GGG ATC TGT CTG AGC TGC CGC	51
	Phe Lys Lys Gly Ile Cys Leu Ser Cys Arg	
	1 5 10	
AAG AAC CGT TGT AAT AGC ATT GGC TAC AAT GCC AAG AAA ATG AGG AAC		99
Lys Asn Arg Cys Asn Ser Ile Gly Tyr Asn Ala Lys Lys Met Arg Asn		
	15 20 25	
AAG AGG AAC AGC AAA ATG TAC CTA AAA ACC CGG GCA GGC ATG CCT TTC		147
Lys Arg Asn Ser Lys Met Tyr Leu Lys Thr Arg Ala Gly Met Pro Phe		
	30 35 40	
AGA GGT AAC CTT CAG TCC CTG GAG TGT CCC TGA GGAAGGCCCT TAATACCTCC		200

Arg Gly Asn Leu Gln Ser Leu Glu Cys Pro	
45 50	
TTCTTAATAC CATGCTGCAG AGCAGGGCAC ATCCTAGCCC AGGAGAAGTG GCCAGCACAA	260
TCCAATCAAA TCGTTGCAA TCAGATTACA CTGTGCATGT CCTAGGAAAG GGAATCTTTA	320
CAAAATAAAC AGTGTGGACC CCTCAAAAAA AAAAAAAGC CGAATTC	367

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 52 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

Phe	Lys	Lys	Gly	Ile	Cys	Leu	Ser	Cys	Arg	Lys	Asn	Arg	Cys	Asn	Ser
1				5					10					15	
Ile	Gly	Tyr	Asn	Ala	Lys	Lys	Met	Arg	Asn	Lys	Arg	Asn	Ser	Lys	Met
			20					25					30		
Tyr	Leu	Lys	Thr	Arg	Ala	Gly	Met	Pro	Phe	Arg	Gly	Asn	Leu	Gln	Ser
		35					40					45			
Leu	Glu	Cys	Pro												
			50												

(2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1382 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

(A) NAME/KEY: CDS

(B) LOCATION: 312..1370

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

GAATTCGGCT TCTACTACTA CTAGGCCACG CGTCGCCTAG TACGGGGGGGG GGGGGGGGGG	60
TCAGCGAGTC CTTGCCTCCC GGCGGCTCAG GACGAGGGCA GATCTCGTTC TGGGGCAAGC	120
CGTTGACACT CGTCCCCTGC CACCGCCCGG GCTCCGTGCC GCCAAGTTTT CATTTTCCAC	180
CTTCTCTGCC TCCAGTCCCC CAGCCCCTGG CCGAGAGAAG GGTCTTACCG GCCGGGATTG	240
CTGGAAACAC CAAGAGGTGG TTTTGTGTTT TTAAACTTC TGTTTCTTGG GAGGGGGTGT	300
GGCGGGGCAG G ATG AGC AAC TCC GTT CCT CTG CTC TGT TTC TGG AGC CTC	350
Met Ser Asn Ser Val Pro Leu Leu Cys Phe Trp Ser Leu	
1 5 10	
TGC TAT TGC TTT GCT GCG GGG AGC CCC GTA CCT TTT GGT CCA GAG GGA	398
Cys Tyr Cys Phe Ala Ala Gly Ser Pro Val Pro Phe Gly Pro Glu Gly	
15 20 25	
CGG CTG GAA GAT AAG CTC CAC AAA CCC AAA GCT ACA CAG ACT GAG GTC	446
Arg Leu Glu Asp Lys Leu His Lys Pro Lys Ala Thr Gln Thr Glu Val	
30 35 40 45	
AAA CCA TCT GTG AGG TTT AAC CTC CGC ACC TCC AAG GAC CCA GAG CAT	494
Lys Pro Ser Val Arg Phe Asn Leu Arg Thr Ser Lys Asp Pro Glu His	
50 55 60	
GAA GGA TGC TAC CTC TCC GTC GGC CAC AGC CAG CCC TTA GAA GAC TGC	542
Glu Gly Cys Tyr Leu Ser Val Gly His Ser Gln Pro Leu Glu Asp Cys	
65 70 75	
AGT TTC AAC ATG ACA GCT AAA ACC TTT TTC ATC ATT CAC GGA TGG ACG	590
Ser Phe Asn Met Thr Ala Lys Thr Phe Phe Ile Ile His Gly Trp Thr	
80 85 90	
ATG AGC GGT ATC TTT GAA AAC TGG CTG CAC AAA CTC GTG TCA GCC CTG	638
Met Ser Gly Ile Phe Glu Asn Trp Leu His Lys Leu Val Ser Ala Leu	
95 100 105	
CAC ACA AGA GAG AAA GAC GCC AAT GTA GTT GTG GTT GAC TGG CTC CCC	686
His Thr Arg Glu Lys Asp Ala Asn Val Val Val Val Asp Trp Leu Pro	
110 115 120 125	
CTG GCC CAC CAG CTT TAC ACG GAT GCG GTC AAT AAT ACC AGG GTG GTG	734

Leu	Ala	His	Gln	Leu	Tyr	Thr	Asp	Ala	Val	Asn	Asn	Thr	Arg	Val	Val		
				130					135					140			
GGA	CAC	AGC	ATT	GCC	AGG	ATG	CTC	GAC	TGG	CTG	CAG	GAG	AAG	GAC	GAT	782	
Gly	His	Ser	Ile	Ala	Arg	Met	Leu	Asp	Trp	Leu	Gln	Glu	Lys	Asp	Asp		
			145					150					155				
TTT	TCT	CTC	GGG	AAT	GTC	CAC	TTG	ATC	GGC	TAC	AGC	CTC	GGA	GCG	CAC	830	
Phe	Ser	Leu	Gly	Asn	Val	His	Leu	Ile	Gly	Tyr	Ser	Leu	Gly	Ala	His		
			160				165					170					
GTG	GCC	GGG	TAT	GCA	GGC	AAC	TTC	GTG	AAA	GGA	ACG	GTG	GGC	CGA	ATC	878	
Val	Ala	Gly	Tyr	Ala	Gly	Asn	Phe	Val	Lys	Gly	Thr	Val	Gly	Arg	Ile		
			175			180					185						
ACA	GGT	TTG	GAT	CCT	GCC	GGG	CCC	ATG	TTT	GAA	GGG	GCC	GAC	ATC	CAC	926	
Thr	Gly	Leu	Asp	Pro	Ala	Gly	Pro	Met	Phe	Glu	Gly	Ala	Asp	Ile	His		
190					195					200				205			
AAG	AGG	CTC	TCT	CCG	GAC	GAT	GCA	GAT	TTT	GTG	GAT	GTC	CTC	CAC	ACC	974	
Lys	Arg	Leu	Ser	Pro	Asp	Asp	Ala	Asp	Phe	Val	Asp	Val	Leu	His	Thr		
				210					215					220			
TAC	ACG	CGT	TCC	TTC	GGC	TTG	AGC	ATT	GGT	ATT	CAG	ATG	CCT	GTG	GGC	1022	
Tyr	Thr	Arg	Ser	Phe	Gly	Leu	Ser	Ile	Gly	Ile	Gln	Met	Pro	Val	Gly		
			225					230					235				
CAC	ATT	GAC	ATC	TAC	CCC	AAT	GGG	GGT	GAC	TTC	CAG	CCA	GGC	TGT	GGA	1070	
His	Ile	Asp	Ile	Tyr	Pro	Asn	Gly	Gly	Asp	Phe	Gln	Pro	Gly	Cys	Gly		
			240				245					250					
CTC	AAC	GAT	GTC	TTG	GGA	TCA	ATT	GCA	TAT	GGA	ACA	ATC	ACA	GAG	GTG	1118	
Leu	Asn	Asp	Val	Leu	Gly	Ser	Ile	Ala	Tyr	Gly	Thr	Ile	Thr	Glu	Val		
			255			260					265						
GTA	AAA	TGT	GAG	CAT	GAG	CGA	GCC	GTC	CAC	CTC	TTT	GTT	GAC	TCT	CTG	1166	
Val	Lys	Cys	Glu	His	Glu	Arg	Ala	Val	His	Leu	Phe	Val	Asp	Ser	Leu		
270					275					280				285			
GTG	AAT	CAG	GAC	AAG	CCG	AGT	TTT	GCC	TTC	CAG	TGC	ACT	GAC	TCC	AAT	1214	
Val	Asn	Gln	Asp	Lys	Pro	Ser	Phe	Ala	Phe	Gln	Cys	Thr	Asp	Ser	Asn		
				290					295					300			
CGC	TTC	AAA	AAG	GGG	ATC	TGT	CTG	AGC	TGC	CGC	AAG	AAC	CGT	TGT	AAT	1262	
Arg	Phe	Lys	Lys	Gly	Ile	Cys	Leu	Ser	Cys	Arg	Lys	Asn	Arg	Cys	Asn		
			305					310					315				
AGC	ATT	GGC	TAC	AAT	GCC	AAG	AAA	ATG	AGG	AAC	AAG	AGG	AAC	AGC	AAA	1310	
Ser	Ile	Gly	Tyr	Asn	Ala	Lys	Lys	Met	Arg	Asn	Lys	Arg	Asn	Ser	Lys		
			320				325					330					
ATG	TAC	CTA	AAA	ACC	CGG	GCA	GGC	ATG	CCT	TTC	AGA	GGT	AAC	CTT	CAG	1358	
Met	Tyr	Leu	Lys	Thr	Arg	Ala	Gly	Met	Pro	Phe	Arg	Gly	Asn	Leu	Gln		
			335			340					345						
TCC	CTG	GAG	TGT	CAAGCCGAAT	TC											1382	
Ser	Leu	Glu	Cys														
350																	

(2) INFORMATION FOR SEQ ID NO:4:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 353 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

Met	Ser	Asn	Ser	Val	Pro	Leu	Leu	Cys	Phe	Trp	Ser	Leu	Cys	Tyr	Cys		
1				5					10					15			
Phe	Ala	Ala	Gly	Ser	Pro	Val	Pro	Phe	Gly	Pro	Glu	Gly	Arg	Leu	Glu		
			20					25					30				
Asp	Lys	Leu	His	Lys	Pro	Lys	Ala	Thr	Gln	Thr	Glu	Val	Lys	Pro	Ser		
			35				40					45					
Val	Arg	Phe	Asn	Leu	Arg	Thr	Ser	Lys	Asp	Pro	Glu	His	Glu	Gly	Cys		
			50			55					60						
Tyr	Leu	Ser	Val	Gly	His	Ser	Gln	Pro	Leu	Glu	Asp	Cys	Ser	Phe	Asn		

65	Met	Thr	Ala	Lys	Thr	85	Phe	Phe	Ile	Ile	His	90	Gly	Trp	Thr	Met	Ser	80	Gly
	Ile	Phe	Glu	Asn	Trp	Leu	His	Lys	Leu	Val	Ser	100	Ala	Leu	His	Thr	Arg		
	Glu	Lys	Asp	Ala	Asn	Val	Val	Val	Val	Asp	Trp	Leu	Pro	Leu	Ala	His			
	Gln	Leu	Tyr	Thr	Asp	Ala	Val	Asn	Asn	Thr	Arg	Val	Val	Gly	His	Ser			
	Ile	Ala	Arg	Met	Leu	Asp	Trp	Leu	Gln	Glu	Lys	115	Asp	Asp	Phe	Ser	Leu		
	Gly	Asn	Val	His	Leu	Ile	Gly	Tyr	Ser	Leu	Gly	120	Ala	His	Val	Ala	Gly		
	Tyr	Ala	Gly	Asn	Phe	Val	Lys	Gly	Thr	Val	Gly	125	Arg	Ile	Thr	Gly	Leu		
	Asp	Pro	Ala	Gly	Pro	Met	Phe	Glu	Gly	Ala	Asp	130	Ile	His	Lys	Arg	Leu		
	Ser	Pro	Asp	Asp	Ala	Asp	Phe	Val	Asp	Val	Leu	135	His	Thr	Tyr	Thr	Arg		
	Ser	Phe	Gly	Leu	Ser	Ile	Gly	Ile	Gln	Met	Pro	140	Val	Gly	His	Ile	Asp		
	Ile	Tyr	Pro	Asn	Gly	Gly	Asp	Phe	Gln	Pro	Gly	145	Cys	Gly	Leu	Asn	Asp		
	Val	Leu	Gly	Ser	Ile	Ala	Tyr	Gly	Thr	Ile	Thr	150	Glu	Val	Val	Lys	Cys		
	Glu	His	Glu	Arg	Ala	Val	His	Leu	Phe	Val	Asp	155	Ser	Leu	Val	Asn	Gln		
	Asp	Lys	Pro	Ser	Phe	Ala	Phe	Gln	Cys	Thr	Asp	160	Ser	Asn	Arg	Phe	Lys		
	Lys	Gly	Ile	Cys	Leu	Ser	Cys	Arg	Lys	Asn	Arg	165	Cys	Asn	Ser	Ile	Gly		
	Tyr	Asn	Ala	Lys	Lys	Met	Arg	Asn	Lys	Arg	Asn	170	Ser	Lys	Met	Tyr	Leu		
	Lys	Thr	Arg	Ala	Gly	Met	Pro	Phe	Arg	Gly	Asn	175	Leu	Gln	Ser	Leu	Glu		
	Cys											180							

(2) INFORMATION FOR SEQ ID NO:5:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2565 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 252..1754

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

GAATTCGCGG	CCGCGTCGAC	GGCGGCTCAG	GACGAGGGCA	GATCTCGTTC	TGGGGCAAGC	60
CGTTGACACT	CGTCCCTGC	CACCGCCCGG	GCTCCGTGCC	GCCAAGTTT	CATTTTCCAC	120
CTTCTCTGCC	TCCAGTCCCC	CAGCCCCTGG	CCGAGAGAAG	GGTCTTACCG	GCCGGGATTG	180
CTGGAACAC	CAAGAGGTGG	TTTTTGTTT	TTAAACTTC	TGTTTCTTGG	GAGGGGTGT	240
GGCGGGGCAG	G ATG AGC AAC TCC GTT CCT CTG CTC TGT TTC TGG AGC CTC					290
	Met Ser Asn Ser Val Pro Leu Leu Cys Phe Trp Ser Leu					
	1 5 10					
TGC TAT TGC TTT GCT GCG GGG AGC CCC GTA CCT TTT GGT CCA GAG GGA						338
Cys Tyr Cys Phe Ala Ala Gly Ser Pro Val Pro Phe Gly Pro Glu Gly						
	15 20 25					
CGG CTG GAA GAT AAG CTC CAC AAA CCC AAA GCT ACA CAG ACT GAG GTC						386
Arg Leu Glu Asp Lys Leu His Lys Pro Lys Ala Thr Gln Thr Glu Val						
	30 35 40 45					
AAA CCA TCT GTG AGG TTT AAC CTC CGC ACC TCC AAG GAC CCA GAG CAT						434
Lys Pro Ser Val Arg Phe Asn Leu Arg Thr Ser Lys Asp Pro Glu His						
	50 55 60					

GAA	GGA	TGC	TAC	CTC	TCC	GTC	GGC	CAC	AGC	CAG	CCC	TTA	GAA	GAC	TGC	482
Glu	Gly	Cys	Tyr	Leu	Ser	Val	Gly	His	Ser	Gln	Pro	Leu	Glu	Asp	Cys	
		65						70					75			
AGT	TTC	AAC	ATG	ACA	GCT	AAA	ACC	TTT	TTC	ATC	ATT	CAC	GGA	TGG	ACG	530
Ser	Phe	Asn	Met	Thr	Ala	Lys	Thr	Phe	Phe	Ile	Ile	His	Gly	Trp	Thr	
	80						85					90				
ATG	AGC	GGT	ATC	TTT	GAA	AAC	TGG	CTG	CAC	AAA	CTC	GTG	TCA	GCC	CTG	578
Met	Ser	Gly	Ile	Phe	Glu	Asn	Trp	Leu	His	Lys	Leu	Val	Ser	Ala	Leu	
	95					100					105					
CAC	ACA	AGA	GAG	AAA	GAC	GCC	AAT	GTA	GTT	GTG	GTT	GAC	TGG	CTC	CCC	626
His	Thr	Arg	Glu	Lys	Asp	Ala	Asn	Val	Val	Val	Val	Asp	Trp	Leu	Pro	
	110				115					120					125	
CTG	GCC	CAC	CAG	CTT	TAC	ACG	GAT	GCG	GTC	AAT	AAT	ACC	AGG	GTG	GTG	674
Leu	Ala	His	Gln	Leu	Tyr	Thr	Asp	Ala	Val	Asn	Asn	Thr	Arg	Val	Val	
			130						135					140		
GGA	CAC	AGC	ATT	GCC	AGG	ATG	CTC	GAC	TGG	CTG	CAG	GAG	AAG	GAC	GAT	722
Gly	His	Ser	Ile	Ala	Arg	Met	Leu	Asp	Trp	Leu	Gln	Glu	Lys	Asp	Asp	
		145						150					155			
TTT	TCT	CTC	GGG	AAT	GTC	CAC	TTG	ATC	GGC	TAC	AGC	CTC	GGA	GCG	CAC	770
Phe	Ser	Leu	Gly	Asn	Val	His	Leu	Ile	Gly	Tyr	Ser	Leu	Gly	Ala	His	
		160					165						170			
GTG	GCC	GGG	TAT	GCA	GGC	AAC	TTC	GTG	AAA	GGA	ACG	GTG	GGC	CGA	ATC	818
Val	Ala	Gly	Tyr	Ala	Gly	Asn	Phe	Val	Lys	Gly	Thr	Val	Gly	Arg	Ile	
	175					180					185					
ACA	GGT	TTG	GAT	CCT	GCC	GGG	CCC	ATG	TTT	GAA	GGG	GCC	GAC	ATC	CAC	866
Thr	Gly	Leu	Asp	Pro	Ala	Gly	Pro	Met	Phe	Glu	Gly	Ala	Asp	Ile	His	
	190				195					200				205		
AAG	AGG	CTC	TCT	CCG	GAC	GAT	GCA	GAT	TTT	GTG	GAT	GTC	CTC	CAC	ACC	914
Lys	Arg	Leu	Ser	Pro	Asp	Asp	Ala	Asp	Phe	Val	Asp	Val	Leu	His	Thr	
				210					215					220		
TAC	ACG	CGT	TCC	TTC	GGC	TTG	AGC	ATT	GGT	ATT	CAG	ATG	CCT	GTG	GGC	962
Tyr	Thr	Arg	Ser	Phe	Gly	Leu	Ser	Ile	Gly	Ile	Gln	Met	Pro	Val	Gly	
			225					230					235			
CAC	ATT	GAC	ATC	TAC	CCC	AAT	GGG	GGT	GAC	TTC	CAG	CCA	GGC	TGT	GGA	1010
His	Ile	Asp	Ile	Tyr	Pro	Asn	Gly	Gly	Asp	Phe	Gln	Pro	Gly	Cys	Gly	
		240					245					250				
CTC	AAC	GAT	GTC	TTG	GGA	TCA	ATT	GCA	TAT	GGA	ACA	ATC	ACA	GAG	GTG	1058
Leu	Asn	Asp	Val	Leu	Gly	Ser	Ile	Ala	Tyr	Gly	Thr	Ile	Thr	Glu	Val	
	255					260					265					
GTA	AAA	TGT	GAG	CAT	GAG	CGA	GCC	GTC	CAC	CTC	TTT	GTT	GAC	TCT	CTG	1106
Val	Lys	Cys	Glu	His	Glu	Arg	Ala	Val	His	Leu	Phe	Val	Asp	Ser	Leu	
	270				275					280					285	
GTG	AAT	CAG	GAC	AAG	CCG	AGT	TTT	GCC	TTC	CAG	TGC	ACT	GAC	TCC	AAT	1154
Val	Asn	Gln	Asp	Lys	Pro	Ser	Phe	Ala	Phe	Gln	Cys	Thr	Asp	Ser	Asn	
				290					295					300		
CGC	TTC	AAA	AAG	GGG	ATC	TGT	CTG	AGC	TGC	CGC	AAG	AAC	CGT	TGT	AAT	1202
Arg	Phe	Lys	Lys	Gly	Ile	Cys	Leu	Ser	Cys	Arg	Lys	Asn	Arg	Cys	Asn	
		305						310					315			
AGC	ATT	GGC	TAC	AAT	GCC	AAG	AAA	ATG	AGG	AAC	AAG	AGG	AAC	AGC	AAA	1250
Ser	Ile	Gly	Tyr	Asn	Ala	Lys	Lys	Met	Arg	Asn	Lys	Arg	Asn	Ser	Lys	
		320					325					330				
ATG	TAC	CTA	AAA	ACC	CGG	GCA	GGC	ATG	CCT	TTC	AGA	GTT	TAC	CAT	TAT	1298
Met	Tyr	Leu	Lys	Thr	Arg	Ala	Gly	Met	Pro	Phe	Arg	Val	Tyr	His	Tyr	
	335					340					345					
CAG	ATG	AAA	ATC	CAT	GTC	TTC	AGT	TAC	AAG	AAC	ATG	GGA	GAA	ATT	GAG	1346
Gln	Met	Lys	Ile	His	Val	Phe	Ser	Tyr	Lys	Asn	Met	Gly	Glu	Ile	Glu	
	350				355					360					365	
CCC	ACC	TTT	TAC	GTC	ACC	CTT	TAT	GGC	ACT	AAT	GCA	GAT	TCC	CAG	ACT	1394
Pro	Thr	Phe	Tyr	Val	Thr	Leu	Tyr	Gly	Thr	Asn	Ala	Asp	Ser	Gln	Thr	
				370					375					380		
CTG	CCA	CTG	GAA	ATA	GTG	GAG	CGG	ATC	GAG	CAG	AAT	GCC	ACC	AAC	ACC	1442
Leu	Pro	Leu	Glu	Ile	Val	Glu	Arg	Ile	Glu	Gln	Asn	Ala	Thr	Asn	Thr	

		385				390			395								
TTC	CTG	GTC	TAC	ACC	GAG	GAG	GAC	TTG	GGA	GAC	CTC	TTG	AAG	ATC	CAG		1490
Phe	Leu	Val	Tyr	Thr	Glu	Glu	Asp	Leu	Gly	Asp	Leu	Leu	Lys	Ile	Gln		
		400					405					410					
CTC	ACC	TGG	GAG	GGG	GCC	TCT	CAG	TCT	TGG	TAC	AAC	CTG	TGG	AAG	GAG		1538
Leu	Thr	Trp	Glu	Gly	Ala	Ser	Gln	Ser	Trp	Tyr	Asn	Leu	Trp	Lys	Glu		
		415				420					425						
TTT	CGC	AGC	TAC	CTG	TCT	CAA	CCC	CGC	AAC	CCC	GGA	CGG	GAG	CTG	AAT		1586
Phe	Arg	Ser	Tyr	Leu	Ser	Gln	Pro	Arg	Asn	Pro	Gly	Arg	Glu	Leu	Asn		
		430			435					440				445			
ATC	AGG	CGC	ATC	CGG	GTG	AAG	TCT	GGG	GAA	ACC	CAG	CGG	AAA	CTG	ACA		1634
Ile	Arg	Arg	Ile	Arg	Val	Lys	Ser	Gly	Glu	Thr	Gln	Arg	Lys	Leu	Thr		
				450					455					460			
TTT	TGT	ACA	GAA	GAC	CCT	GAG	AAC	ACC	AGC	ATA	TCC	CCA	GGC	CGG	GAG		1682
Phe	Cys	Thr	Glu	Asp	Pro	Glu	Asn	Thr	Ser	Ile	Ser	Pro	Gly	Arg	Glu		
			465					470					475				
CTC	TGG	TTT	CGC	AAG	TGT	CGG	GAT	GGC	TGG	AGG	ATG	AAA	AAC	GAA	ACC		1730
Leu	Trp	Phe	Arg	Lys	Cys	Arg	Asp	Gly	Trp	Arg	Met	Lys	Asn	Glu	Thr		
		480					485				490						
AGT	CCC	ACT	GTG	GAG	CTT	CCC	TGA	GGGTGCCCGG	GCAAGTCTTG	CCAGCAAGGC							1784
Ser	Pro	Thr	Val	Glu	Leu	Pro											
		495				500											
AGCAAGACTT	CCTGCTATCC	AAGCCCATGG	AGGAAAAGTTA	CTGCTGAGGA	CCCACCCAAT												1844
GGAAGGATTC	TTCTCAGCCT	TGACCCTGGA	GCACTGGGAA	CAACTGGTCT	CCTGTGATGG												1904
CTGGGACTCC	TCGCGGGAGG	GGACTGCGCT	GCTATAGCTC	TTGCTGCCTC	TCTTGAATAG												1964
CTCTAACTCC	AAACCTCTGT	CCACACCTCC	AGAGCACCAA	GTCCAGATTT	GTGTGTAAGC												2024
AGCTGGGTGC	CTGGGGCCTC	TCGTGCACAC	TGGATTGGTT	TCTCAGTTGC	TGGGCGAGCC												2084
TGTACTCTGC	CTGACGAGGA	ACGCTGGCTC	CGAAGAGGCC	CTGTGTAGAA	GGCTGTCAGC												2144
TGCTCAGCCT	GCTTTGAGCC	TCAGTGAGAA	GTCCTTCCGA	CAGGAGCTGA	CTCATGTCTAG												2204
GATGGCAGGC	CTGGTATCTT	GCTCGGGCCC	TGGCTGTTGG	GGTTCTCATG	GGTTGCACTG												2264
ACCATACTGC	TTACGTCTTA	GCCATTCCGT	CCTGCTCCCC	AGCTCACTCT	CTGAAGCACA												2324
CATCATTGGC	TTTCCTATTT	TTCTGTTCAT	TTTTTAATTG	AGCAAATGTC	TATTGAACAC												2384
TTAAATTAAT	TTAGAATGTG	GTAATGGACA	TATTACTGAG	CCTCTCCATT	TGGAACCCAG												2444
TGGAGTTGGG	ATTTCTAGAC	CCTCTTTCTG	TTTGGATGGT	GTATGTGTAT	ATGCATGGGG												2504
AAAGGCACCT	GGGGCCTGGG	GGAGGCTATA	GGATATAAGC	AGTCGACGCG	GCCGCGAATT												2564
C																	2565

(2) INFORMATION FOR SEQ ID NO:6:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 500 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

Met	Ser	Asn	Ser	Val	Pro	Leu	Leu	Cys	Phe	Trp	Ser	Leu	Cys	Tyr	Cys
1				5					10					15	
Phe	Ala	Ala	Gly	Ser	Pro	Val	Pro	Phe	Gly	Pro	Glu	Gly	Arg	Leu	Glu
			20					25					30		
Asp	Lys	Leu	His	Lys	Pro	Lys	Ala	Thr	Gln	Thr	Glu	Val	Lys	Pro	Ser
		35					40					45			
Val	Arg	Phe	Asn	Leu	Arg	Thr	Ser	Lys	Asp	Pro	Glu	His	Glu	Gly	Cys
	50				55				60						
Tyr	Leu	Ser	Val	Gly	His	Ser	Gln	Pro	Leu	Glu	Asp	Cys	Ser	Phe	Asn
	65			70					75					80	
Met	Thr	Ala	Lys	Thr	Phe	Phe	Ile	Ile	His	Gly	Trp	Thr	Met	Ser	Gly
			85					90					95		
Ile	Phe	Glu	Asn	Trp	Leu	His	Lys	Leu	Val	Ser	Ala	Leu	His	Thr	Arg
			100					105					110		
Glu	Lys	Asp	Ala	Asn	Val	Val	Val	Val	Asp	Trp	Leu	Pro	Leu	Ala	His
		115				120					125				
Gln	Leu	Tyr	Thr	Asp	Ala	Val	Asn	Asn	Thr	Arg	Val	Val	Gly	His	Ser
	130				135						140				
Ile	Ala	Arg	Met	Leu	Asp	Trp	Leu	Gln	Glu	Lys	Asp	Asp	Phe	Ser	Leu
	145			150					155					160	
Gly	Asn	Val	His	Leu	Ile	Gly	Tyr	Ser	Leu	Gly	Ala	His	Val	Ala	Gly

35 40 45
 GGG ATC TGT CTC AGC TGC CGG AAG AAC CGC TGT AAC GGC ATC GGC TAC 192
 Gly Ile Cys Leu Ser Cys Arg Lys Asn Arg Cys Asn Gly Ile Gly Tyr
 50 55 60

AAT GCT AAG AAG ACG AGG AAT AAG AGG AAC ACC 225
 Asn Ala Lys Lys Thr Arg Asn Lys Arg Asn Thr
 65 70 75

(2) INFORMATION FOR SEQ ID NO:8:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 75 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

Leu Gly Ser Ile Ala Tyr Gly Thr Ile Ala Glu Val Val Lys Cys Glu
 1 5 10 15
 His Glu Arg Ala Val His Leu Phe Val Asp Ser Leu Val Asn Gln Asp
 20 25 30
 Lys Pro Ser Phe Ala Phe Gln Cys Thr Asp Ser Asn Arg Phe Lys Lys
 35 40 45
 Gly Ile Cys Leu Ser Cys Arg Lys Asn Arg Cys Asn Gly Ile Gly Tyr
 50 55 60
 Asn Ala Lys Lys Thr Arg Asn Lys Arg Asn Thr
 65 70 75

(2) INFORMATION FOR SEQ ID NO:9:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 475 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

Met Glu Ser Lys Ala Leu Leu Val Leu Thr Leu Ala Val Trp Leu Gln
 1 5 10 15
 Ser Leu Thr Ala Ser Arg Gly Gly Val Ala Ala Ala Asp Gln Arg Arg
 20 25 30
 Asp Phe Ile Asp Ile Glu Ser Lys Phe Ala Leu Arg Thr Pro Glu Asp
 35 40 45
 Thr Ala Glu Asp Thr Cys His Leu Ile Pro Gly Val Ala Glu Ser Val
 50 55 60
 Ala Thr Cys His Phe Asn His Ser Ser Lys Thr Phe Met Val Ile His
 65 70 75 80
 Gly Trp Thr Val Thr Gly Met Tyr Glu Ser Trp Val Pro Lys Leu Val
 85 90 95
 Ala Ala Leu Tyr Lys Arg Glu Pro Asp Ser Asn Val Ile Val Val Asp
 100 105 110
 Trp Leu Ser Arg Ala Gln Glu His Tyr Pro Val Ser Ala Gly Tyr Thr
 115 120 125
 Lys Leu Val Gly Gln Asp Val Ala Arg Phe Ile Asn Trp Met Glu Glu
 130 135 140
 Glu Phe Asn Tyr Pro Leu Asp Asn Val His Leu Leu Gly Tyr Ser Leu
 145 150 155 160
 Gly Ala His Ala Ala Gly Ile Ala Gly Ser Leu Thr Asn Lys Lys Val
 165 170 175
 Asn Arg Ile Thr Gly Leu Asp Pro Ala Gly Pro Asn Phe Glu Tyr Ala
 180 185 190
 Glu Ala Pro Ser Arg Leu Ser Pro Asp Asp Ala Asp Phe Val Asp Val
 195 200 205
 Leu His Thr Phe Thr Arg Gly Ser Pro Gly Arg Ser Ile Gly Ile Gln

210	215	220
Lys Pro Val Gly His Val Asp Ile Tyr Pro Asn Gly Gly Thr Phe Gln		
225	230	235
Pro Gly Cys Asn Ile Gly Glu Ala Ile Arg Val Ile Ala Glu Arg Gly		
	245	250
Leu Gly Asp Val Asp Gln Leu Val Lys Cys Ser His Glu Arg Ser Ile		
	260	265
His Leu Phe Ile Asp Ser Leu Leu Asn Glu Glu Asn Pro Ser Lys Ala		
	275	280
Tyr Arg Cys Ser Ser Lys Glu Ala Phe Glu Lys Gly Leu Cys Leu Ser		
	290	295
Cys Arg Lys Asn Arg Cys Asn Asn Leu Gly Tyr Glu Ile Asn Lys Val		
305	310	315
Arg Ala Lys Arg Ser Ser Lys Met Tyr Leu Lys Thr Arg Ser Gln Met		
	325	330
Pro Tyr Lys Val Phe His Tyr Gln Val Lys Ile His Phe Ser Gly Thr		
	340	345
Glu Ser Glu Thr His Thr Asn Gln Ala Phe Glu Ile Ser Leu Tyr Gly		
	355	360
Thr Val Ala Glu Ser Glu Asn Ile Pro Phe Thr Leu Pro Glu Val Ser		
370	375	380
Thr Asn Lys Thr Tyr Ser Phe Leu Ile Tyr Thr Glu Val Asp Ile Gly		
385	390	395
Glu Leu Leu Met Leu Lys Leu Lys Trp Lys Ser Asp Ser Tyr Phe Ser		
	405	410
Trp Ser Asp Trp Trp Ser Ser Pro Gly Phe Ala Ile Gln Lys Ile Arg		
	420	425
Val Lys Ala Gly Glu Thr Gln Lys Lys Val Ile Phe Cys Ser Arg Glu		
	435	440
Lys Val Ser His Leu Gln Lys Gly Lys Ala Pro Ala Val Phe Val Lys		
	450	455
Cys His Asp Lys Ser Leu Asn Lys Lys Ser Gly		460
465	470	475

(2) INFORMATION FOR SEQ ID NO:10:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 499 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

Met Asp Thr Ser Pro Leu Cys Phe Ser Ile Leu Leu Val Leu Cys Ile	
1	5
Phe Ile Gln Ser Ser Ala Leu Gly Gln Ser Leu Lys Pro Glu Pro Phe	
	20
Gly Arg Arg Ala Gln Ala Val Glu Thr Asn Lys Thr Leu His Glu Met	
	35
Lys Thr Arg Phe Leu Leu Phe Gly Glu Thr Asn Gln Gly Cys Gln Ile	
	50
Arg Ile Asn His Pro Asp Thr Leu Gln Glu Cys Gly Phe Asn Ser Ser	
65	70
Leu Pro Leu Val Met Ile Ile His Gly Trp Ser Val Asp Gly Val Leu	
	85
Glu Asn Trp Ile Trp Gln Met Val Ala Ala Leu Lys Ser Gln Pro Ala	
	100
Gln Pro Val Asn Val Gly Leu Val Asp Trp Ile Thr Leu Ala His Asp	
	115
His Tyr Thr Ile Ala Val Arg Asn Thr Arg Leu Val Gly Lys Glu Val	
	130
Ala Ala Leu Leu Arg Trp Leu Glu Glu Ser Val Gln Leu Ser Arg Ser	
145	150
His Val His Leu Ile Gly Tyr Ser Leu Gly Ala His Val Ser Gly Phe	
	165
	170
	175

Ala	Gly	Ser	Ser	Ile	Gly	Gly	Thr	His	Lys	Ile	Gly	Arg	Ile	Thr	Gly
			180					185					190		
Leu	Asp	Ala	Ala	Gly	Pro	Leu	Phe	Glu	Gly	Ser	Ala	Pro	Ser	Asn	Arg
		195					200					205			
Leu	Ser	Pro	Asp	Asp	Ala	Asn	Phe	Val	Asp	Ala	Ile	His	Thr	Phe	Thr
	210					215					220				
Arg	Glu	His	Met	Gly	Leu	Ser	Val	Gly	Ile	Lys	Gln	Pro	Ile	Gly	His
	225				230					235					240
Tyr	Asp	Phe	Tyr	Pro	Asn	Gly	Gly	Ser	Phe	Gln	Pro	Gly	Cys	His	Phe
				245					250					255	
Leu	Glu	Leu	Tyr	Arg	His	Ile	Ala	Gln	His	Gly	Phe	Asn	Ala	Ile	Thr
			260					265					270		
Gln	Thr	Ile	Lys	Cys	Ser	His	Glu	Arg	Ser	Val	His	Leu	Phe	Ile	Asp
		275					280					285			
Ser	Leu	Leu	His	Ala	Gly	Thr	Gln	Ser	Met	Ala	Tyr	Pro	Cys	Gly	Asp
	290					295					300				
Met	Asn	Ser	Phe	Ser	Gln	Gly	Leu	Cys	Leu	Ser	Cys	Lys	Lys	Gly	Arg
	305				310					315					320
Cys	Asn	Thr	Leu	Gly	Tyr	His	Val	Arg	Gln	Glu	Pro	Arg	Ser	Lys	Ser
				325					330					335	
Lys	Arg	Leu	Phe	Leu	Val	Thr	Arg	Ala	Gln	Ser	Pro	Phe	Lys	Val	Tyr
			340					345					350		
His	Tyr	Gln	Leu	Lys	Ile	Gln	Phe	Ile	Asn	Gln	Thr	Glu	Thr	Pro	Ile
		355					360						365		
Gln	Thr	Thr	Phe	Thr	Met	Ser	Leu	Leu	Gly	Thr	Lys	Glu	Lys	Met	Gln
	370					375					380				
Lys	Ile	Pro	Ile	Thr	Leu	Gly	Lys	Gly	Ile	Ala	Ser	Asn	Lys	Thr	Tyr
	385				390					395					400
Ser	Phe	Leu	Ile	Thr	Leu	Asp	Val	Asp	Ile	Gly	Glu	Leu	Ile	Met	Ile
				405					410					415	
Lys	Phe	Lys	Trp	Glu	Asn	Ser	Ala	Val	Trp	Ala	Asn	Val	Trp	Asp	Thr
			420					425					430		
Val	Gln	Thr	Ile	Ile	Pro	Trp	Ser	Thr	Gly	Pro	Arg	His	Ser	Gly	Leu
		435					440					445			
Val	Leu	Lys	Thr	Ile	Arg	Val	Lys	Ala	Gly	Glu	Thr	Gln	Gln	Arg	Met
	450					455					460				
Thr	Phe	Cys	Ser	Glu	Asn	Thr	Asp	Asp	Leu	Leu	Leu	Arg	Pro	Thr	Gln
	465				470					475					480
Glu	Lys	Ile	Phe	Val	Lys	Cys	Glu	Ile	Lys	Ser	Lys	Thr	Ser	Lys	Arg
				485					490					495	
Lys	Ile	Arg													

(2) INFORMATION FOR SEQ ID NO:11:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 465 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

Met	Leu	Pro	Leu	Trp	Thr	Leu	Ser	Leu	Leu	Leu	Gly	Ala	Val	Ala	Gly
1				5				10						15	
Lys	Glu	Val	Cys	Tyr	Glu	Arg	Leu	Gly	Cys	Phe	Ser	Asp	Asp	Ser	Pro
			20					25					30		
Trp	Ser	Gly	Ile	Thr	Glu	Arg	Pro	Leu	His	Ile	Leu	Pro	Trp	Ser	Pro
		35					40					45			
Lys	Asp	Val	Asn	Thr	Arg	Phe	Leu	Leu	Tyr	Thr	Asn	Glu	Asn	Pro	Asn
	50					55					60				
Asn	Phe	Gln	Glu	Val	Ala	Asp	Ser	Ser	Ser	Ser	Ile	Ser	Gly	Ser	Asn
	65				70					75					80
Phe	Lys	Thr	Asn	Arg	Lys	Thr	Arg	Phe	Ile	Ile	His	Gly	Phe	Ile	Asp
			85					90					95		
Lys	Gly	Glu	Glu	Asn	Trp	Leu	Ala	Asn	Val	Cys	Lys	Asn	Leu	Phe	Lys
		100						105					110		
Val	Glu	Ser	Val	Asn	Cys	Ile	Cys	Val	Asp	Trp	Lys	Gly	Gly	Ser	Arg

(ii) MOLECULE TYPE: other nucleic acid
(A) DESCRIPTION: /desc = "Oligonucleotide"
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:
TTTTTTTTTT TGA 13

(2) INFORMATION FOR SEQ ID NO:14:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 10 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: other nucleic acid
(A) DESCRIPTION: /desc = "Oligonucleotide"
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:
GATCAATCGC 10

(2) INFORMATION FOR SEQ ID NO:15:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 23 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: other nucleic acid
(A) DESCRIPTION: /desc = "Oligonucleotide"
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:
TAGGACATGC ACAGTGTAAT CTG 23

(2) INFORMATION FOR SEQ ID NO:16:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: other nucleic acid
(A) DESCRIPTION: /desc = "Oligonucleotide"
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:
GATTGTGCTG GCCACTTCTC 20

(2) INFORMATION FOR SEQ ID NO:17:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 19 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: other nucleic acid
(A) DESCRIPTION: /desc = "Oligonucleotide"
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:17:
GACACTCCAG GGACTGAAG 19

(2) INFORMATION FOR SEQ ID NO:18:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 48 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: other nucleic acid
(A) DESCRIPTION: /desc = "Oligonucleotide"
(ix) FEATURE:
(A) NAME/KEY: modified_base
(B) LOCATION: 36
(D) OTHER INFORMATION: /mod_base= i
(ix) FEATURE:
(A) NAME/KEY: modified_base
(B) LOCATION: 37
(D) OTHER INFORMATION: /mod_base= i

(ix) FEATURE:
 (A) NAME/KEY: modified_base
 (B) LOCATION: 41
 (D) OTHER INFORMATION: /mod_base= i

(ix) FEATURE:
 (A) NAME/KEY: modified_base
 (B) LOCATION: 42
 (D) OTHER INFORMATION: /mod_base= i

(ix) FEATURE:
 (A) NAME/KEY: modified_base
 (B) LOCATION: 46
 (D) OTHER INFORMATION: /mod_base= i

(ix) FEATURE:
 (A) NAME/KEY: modified_base
 (B) LOCATION: 47
 (D) OTHER INFORMATION: /mod_base= i

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:18:
 CUACUACUAC UAGGCCACGC GTCGACTAGT ACGGGNNGGG NNGGGNNG 48

(2) INFORMATION FOR SEQ ID NO:19:
 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 28 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear
 (ii) MOLECULE TYPE: other nucleic acid
 (A) DESCRIPTION: /desc = "Oligonucleotide"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:19:
 CACACACAGG CCACGCGTCG ACTAGTAC 28

(2) INFORMATION FOR SEQ ID NO:20:
 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 24 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear
 (ii) MOLECULE TYPE: other nucleic acid
 (A) DESCRIPTION: /desc = "Oligonucleotide"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:20:
 ACCACCATGG AGAGCAAAGC CCTG 24

(2) INFORMATION FOR SEQ ID NO:21:
 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 25 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear
 (ii) MOLECULE TYPE: other nucleic acid
 (A) DESCRIPTION: /desc = "Oligonucleotide"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:21:
 CCAGTTTCAG CCTGACTTCT TATTC 25

(2) INFORMATION FOR SEQ ID NO:22:
 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 21 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear
 (ii) MOLECULE TYPE: other nucleic acid
 (A) DESCRIPTION: /desc = "Oligonucleotide"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:22:
 GGCTGTGGAC TCAACGATGT C 21

(2) INFORMATION FOR SEQ ID NO:23:
 (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 22 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear
 (ii) MOLECULE TYPE: other nucleic acid
 (A) DESCRIPTION: /desc = "Oligonucleotide"
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:23:
 CCGGGTGGGT AGGTACATTT TG 22

(2) INFORMATION FOR SEQ ID NO:24:
 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 25 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear
 (ii) MOLECULE TYPE: other nucleic acid
 (A) DESCRIPTION: /desc = "Oligonucleotide"
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:24:
 GGGGGTGACT TCCAGCCAGG CTGTG 25

(2) INFORMATION FOR SEQ ID NO:25:
 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 25 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear
 (ii) MOLECULE TYPE: other nucleic acid
 (A) DESCRIPTION: /desc = "Oligonucleotide"
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:25:
 AACTCTGAAA GGCATGCCTG CCCGG 25

(2) INFORMATION FOR SEQ ID NO:26:
 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 26 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear
 (ii) MOLECULE TYPE: other nucleic acid
 (A) DESCRIPTION: /desc = "Oligonucleotide"
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:26:
 TGAAGGTCGG AGTCAACGGA TTTGGT 26

(2) INFORMATION FOR SEQ ID NO:27:
 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 24 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear
 (ii) MOLECULE TYPE: other nucleic acid
 (A) DESCRIPTION: /desc = "Oligonucleotide"
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:27:
 CATGTGGGCC ATGAGGTCCA CCAC 24